MICROARRAY-BASED SUBTRACTIVE HYBRIDIZATION

Abstract of the Disclosure

The present invention relates to a highly efficient, high-throughput method for the identification and elimination of redundancy in a population of nucleic acid molecules using microarrays. This method involves a reiterative subtraction protocol that creates a library that becomes more biased toward unknown genes with each successive round. The removal of repetitive and previously characterized nucleic acids from the library allows the identification of low-abundance mRNA from sources of interest and enhances the rate of novel gene discovery. The present invention is also useful for the removal of contaminating nucleic acids from cloning libraries.

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